

Express Mail No.: EL615430215US

FORM PTO-1449

LIST OF PATENTS AND OTHER ITEMS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT

(Use several sheets if necessary)

ATTY. DOCKET NO.

01561.0002.CPUS01

SERIAL NO.

09/767,460

APPLICANT:

Arnold J. Mandell, et al.

FILING DATE:

1/23/01

GROUP:

1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
			None			

RECEIVED

OCT 15 2000

TECH CENTER 1000-1000

FOREIGN PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	TRANSLATION YES	TRANSLATION NO
			None				

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, etc.)

AS	AA	Mandell, A.J. (1984) Non-equilibrium behavior of some brain enzyme and receptor systems. Ann. Rev. Pharm. Toxicol. 24:237-274
AS	AB	Mandell, A.J., Russo, P.V. and Blomgren, B.W. (1987) Complex hydrophobic sequence transformation predicts mutual recognition by polypeptides and proteins. Ann. N.Y. Acad. Sci. 504:88-118.
AS	AC	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Mode matches and their locations in the hydrophobic free energy sequences of peptide ligands and their receptor eigenfunctions. Proc. Natl. Acad. Sci. 94:13576-13581.
AS	AD	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Wavelet transformation of protein hydrophobicity sequences suggests their memberships in structural families. Physica A224: 254-262.

EXAMINER: Initial reference is considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include a copy of this form with next communication to applicant

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JB	AE	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Hydrophobic free energy eigenfunctions help define continuous wavelet transformations of amino acid sequences of protein families. Proc. Intl. (Fermi) Sch. Phys. CXXXIV, 175-192.
JB	AF	Di Marzo, E.A. and Mandell, A.J. (1997) Phase transition behavior of a linear macromolecule threading a membrane. J. Chem. Physics 107:5510-5514.
JB	AG	Mandell, A.J., Owens, M.J. Selz, K.A., Morgan, W.N., Schlesinger, M.F. and Nemeroff, C.G. (1998) Mode matches in hydrophobic free energy eigenfunctions predict protein-protein interactions. Biopolymers 46:89-101.
JB	AH	Selz, K.A., Mandell, A.J., and Shlesinger, M.F. (1998) Hydrophobic free energy eigenfunctions of pore, channel and transporter proteins contain B-burst patterns. Biophysical J. 7:2332-2342.
JB	AI	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1998) Transformational homologies in amino acid sequences suggest membership in protein families. J. Stat. Phys. 93:673-697.
JB	AJ	Mandell, A.J., Selz, K.A., Shlesinger, M.F., and Kuhar, M.J. (1999) Linear and entropic transformations of the hydrophobic free energy sequence help characterize a novel brain polyprotein: CART. In (M.T. Batchelor and L. Wille, eds.), Statistical Physics on the Eve of the Twenty-First Century. World Scientific, NJ, pp. 131-152.
JB	AK	White, Stephen H. and Jacobs, Russell E. (1994) Global Statistics of Protein Sequences: Implications for the Origin, Evolution, and Prediction of Structure. Annu. Rev. Biophys. Chem. Struct. 23:407-430. Manavalan, P. and Ponnuswamy, P.K. (1978) Statistical distribution of hydrophobic residues along the length of protein chains. Biophys. J., Volume 57 pp. 911-921. White, Stephen H. and Jacobs, Russell E. (1994) Global Statistics of Protein Sequences: Implications for the Origin, Evolution, and Prediction of Structure. Annu. Rev. Biophys. Chem. Struct. 23:407-430. <i>Reference not provided</i>
JB	AL	Doyle, P.M. (1995) Combinatorial Chemistry in the Discovery and Development of Drugs. J. Chem. Tech. Biotechnol. 64:317-324.
JB	AM	Gordon, E.M., Barrett, R.W., Dower, W.J., Fodor, S.P.A. and Gallop, M.A. (1994) Applications of Combinatorial Technologies to Drug Discovery. 2. Combinatorial Organic Synthesis, Library Screening Strategies, and Future Directions. J. Med. Chem. 37(10):1385-1401.
JB	AN	
JB	AO	Houghton, R.A. (1993) The Broad Utility of Soluble Peptide Libraries for Drug Discovery. Gene 137:7-11.

SP-835461

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Mandell, Arnold J., Selz, Karen A., and Shlesinger, Michael F. Predicting Peptide-Receptor, Peptide-Protein, and Chaperone-Protein Binding using patterns in amino acid hydrophobic free energy sequences, The Journal of Physical Chemistry B, Vol 104, No. 16, pgs 3953-3959

AP

John B. Bruner 29 October 2003

SD-82846-1

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